

600-1-259 SEQUENCES

1
2
3
4 (SEQ ID No:1) LEVLFQGP
5
6
7 (SEQ ID No:2) EAIYAAPFAKKK
8
9
10 (SEQ ID No:3) 5' primer AAA AGA AAA AAA GGC GGC CGC TCG GAT CTG
11 ATC GAA GGT CGT TGT GCG GGC AAC TTC GAC TCG G
12
13
14 (SEQ ID No:4) 3' primer GCA AAC TGG CTC TTC CGC AGC CGC TGA AGT
15 CCT CAT CGG G
16
17
18 (SEQ ID No:5) MASSRVDGGRSDLIIEGRC
19
20
21 (SEQ ID No:6) CGK-[Dapa(Fl)]-GLEVLFQGPVRKG-[K^E-(Biotin)]-G-NH₂ (Cys-Fl-
22 PS-Biotin)
23
24
25 (SEQ ID No:7) PPPALPPKRRR-NH₂
26
27
28 (SEQ ID No:8)
29 Rh-KRGCAGNFDSEERSSWYWGRLSRQEAVALLQGQRHGVFLVRDSSTSPGD
30 YVLSVSENSRVSHYIINSSGPRPP
31 VPPSPAQPPPGVSPSRLRIGDQEFDSLPALEFYKIHLYDTTTTLIEPVARSRQGS
32 GVILRQEEAEYVRALFDFNGN
33 DEEDLPFKKGDILRIRDKPEEQWWNAEDSEGKRGMPVPYVEKYRPASASVS
34 ALIGGNQEGSHPPQLGGPEPGPYA
35 QPSVNTPLPNLQNGPIYARVIQKRVPNAYDKTALALEVGELVKVTKINVSGQ
36 WEGECNGKRGHFPFTHVRLLDQQN
37 PDEDFSGCGKDapa(Fl)GLEVLFQ
38
39
40 (SEQ ID No:9)
41 Rh-KRGCAGNFDSEERSSWYWGRLSRQEAVALLQGQRHGVFLVRDSSTSPGD
42 YVLSVSENSRVSHYIINSSGPRPP
43 VPPSPAQPPPGVSPSRLRIGDQEFDSLPALEFYKIHLYDTTTTLIEPVARSRQGS
44 GVILRQEEAEYVRALFDFNGN
45 DEEDLPFKKGDILRIRDKPEEQWWNAEDSEGKRGMPVPYVEKYRPASASVS
46 ALIGGNQEGSHPPQLGGPEPGPYA
47 QPSVNTPLPNLQNGPIYARVIQKRVPNAYDKTALALEVGELVKVTKINVSGQ
48 WEGECNGKRGHFPFTHVRLLDQQN
49 PDEDFSGCGKDapa(Fl)GLEVLFQGPVRKGK(Biotin)G
50

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50

Sub
a